

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: TAKAHASHI, Tohru
SERIZAWA, Nobufusa
KOISHI, Ryuta
KAWASHIMA, Ichiro
- (ii) TITLE OF INVENTION: EXPRESSION SYSTEMS UTILIZING
AUTOLYZING FUSION PROTEINS
AND A NOVEL REDUCING POLYPEPTIDE
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Frishhauf, Holtz, Goodman, Langer & Chick, P.C.
(B) STREET: 767 Third Avenue-25th Floor
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10017-2023
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/500,635
(B) FILING DATE: 11-JUL-1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 6-161053
(B) FILING DATE: 13-JUL-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 6-218392
(B) FILING DATE: 13-SEP-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 6-303809
(B) FILING DATE: 07-DEC-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Goodman, Herbert
(B) REGISTRATION NUMBER: 17081
(C) REFERENCE/DOCKET NUMBER: 950376/HG
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 319-4900
(B) TELEFAX: (212) 319-5101
(C) TELEX: 236268

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

00042347 "042501

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Clover Yellow Vein Virus

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1320

(D) OTHER INFORMATION:

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 10..1311

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAG	TTC	CAA	GGG	AAA	AGT	AAG	AGA	ACA	AGA	CAA	AAG	TTG	AAG	TTC	AGA	48
Lys	Phe	Gln	Gly	Lys	Ser	Lys	Arg	Thr	Arg	Gln	Lys	Leu	Lys	Phe	Arg	
1				5					10					15		
GCG	GCA	AGA	GAC	ATG	AAG	GAT	CGT	TAT	GAA	GTG	CAT	GCC	GAT	GAG	GGG	96
Ala	Ala	Arg	Asp	Met	Lys	Asp	Arg	Tyr	Glu	Val	His	Ala	Asp	Glu	Gly	
			20					25					30			
ACT	TTA	GTG	GAA	AAT	TTT	GGA	ACT	CGT	TAT	TCA	AAG	AAA	GGC	AAG	ACA	144
Thr	Leu	Val	Glu	Asn	Phe	Gly	Thr	Arg	Tyr	Ser	Lys	Lys	Gly	Lys	Thr	
		35					40						45			
AAA	GGT	ACT	GTT	GTG	GGT	TTG	GGT	GCA	AAA	ACA	AGA	CGG	TTC	ACT	AAC	192
Lys	Gly	Thr	Val	Val	Gly	Leu	Gly	Ala	Lys	Thr	Arg	Arg	Phe	Thr	Asn	
		50				55					60					
ATG	TAT	GGT	TTT	GAC	CCC	ACG	GAG	TAT	TCA	TTT	GCT	AGG	TAT	CTT	GAT	240
Met	Tyr	Gly	Phe	Asp	Pro	Thr	Glu	Tyr	Ser	Phe	Ala	Arg	Tyr	Leu	Asp	
	65				70					75					80	
CCA	ATC	ACG	GGT	GCA	ACA	TTG	GAT	GAA	ACC	CCA	ATT	CAC	AAT	GTA	AAT	288
Pro	Ile	Thr	Gly	Ala	Thr	Leu	Asp	Glu	Thr	Pro	Ile	His	Asn	Val	Asn	
				85					90					95		
TTG	GTT	GCT	GAG	CAT	TTT	GGC	GAC	ATA	AGG	CTT	GAT	ATG	GTT	GAC	AAG	336
Leu	Val	Ala	Glu	His	Phe	Gly	Asp	Ile	Arg	Leu	Asp	Met	Val	Asp	Lys	
		100					105						110			
GAG	TTA	CTT	GAC	AAA	CAG	CAC	TTA	TAC	CTC	AAG	AGA	CCA	ATA	GAA	TGT	384
Glu	Leu	Leu	Asp	Lys	Gln	His	Leu	Tyr	Leu	Lys	Arg	Pro	Ile	Glu	Cys	
		115					120					125				
TAC	TTT	GTA	AAG	GAT	GCT	GGT	CAG	AAG	GTG	ATG	AGG	ATT	GAT	CTA	ACA	432
Tyr	Phe	Val	Lys	Asp	Ala	Gly	Gln	Lys	Val	Met	Arg	Ile	Asp	Leu	Thr	
		130				135					140					
CCC	CAC	AAC	CCA	TTG	TTG	GCA	AGC	GAT	GTT	AGC	ACA	ACC	ATA	ATG	GGT	480
Pro	His	Asn	Pro	Leu	Leu	Ala	Ser	Asp	Val	Ser	Thr	Thr	Ile	Met	Gly	
				145		150				155					160	

TAT	CCT	GAG	AGA	GAA	GGT	GAA	CTC	CGT	CAA	ACT	GGA	AAG	GCA	AGG	TTA	528
Tyr	Pro	Glu	Arg	Glu	Gly	Glu	Leu	Arg	Gln	Thr	Gly	Lys	Ala	Arg	Leu	
				165					170					175		
GTC	GAC	CCA	TCA	GAG	TTG	CCC	GCG	CGG	AAT	GAG	GAT	ATT	GAT	GCA	GAG	576
Val	Asp	Pro	Ser	Glu	Leu	Pro	Ala	Arg	Asn	Glu	Asp	Ile	Asp	Ala	Glu	
			180					185					190			
TTT	GAG	AGT	CTA	AAT	CGC	ATA	AGT	GGT	TTG	CGC	GAC	TAT	AAT	CCC	ATT	624
Phe	Glu	Ser	Leu	Asn	Arg	Ile	Ser	Gly	Leu	Arg	Asp	Tyr	Asn	Pro	Ile	
		195					200					205				
TCA	CAA	AAT	GTT	TGC	TTG	CTA	ACA	AAT	GAG	TCA	GAA	GGC	CAT	AGA	GAG	672
Ser	Gln	Asn	Val	Cys	Leu	Leu	Thr	Asn	Glu	Ser	Glu	Gly	His	Arg	Glu	
	210					215					220					
AAG	ATG	TTT	GGA	ATT	GGA	TAT	GGT	TCA	GTG	ATC	ATT	ACA	AAT	CAA	CAT	720
Lys	Met	Phe	Gly	Ile	Gly	Tyr	Gly	Ser	Val	Ile	Ile	Thr	Asn	Gln	His	
225				230					235						240	
CTG	TTC	AGA	AGG	AAT	AAT	GGG	GAG	TTA	TCA	ATT	CAA	TCC	AAG	CAT	GGC	768
Leu	Phe	Arg	Arg	Asn	Asn	Gly	Glu	Leu	Ser	Ile	Gln	Ser	Lys	His	Gly	
				245					250					255		
TAC	TTC	AGA	TGC	CGC	AAC	ACC	ACA	AGC	TTG	AAG	ATG	CTG	CCT	TTG	GAG	816
Tyr	Phe	Arg	Cys	Arg	Asn	Thr	Thr	Ser	Leu	Lys	Met	Leu	Pro	Leu	Glu	
			260					265					270			
GGA	CAT	GAC	ATT	TTG	TTG	ATT	CAG	TTA	CCA	AGG	GAC	TTT	CCA	GTG	TTT	864
Gly	His	Asp	Ile	Leu	Leu	Ile	Gln	Leu	Pro	Arg	Asp	Phe	Pro	Val	Phe	
		275					280					285				
CCA	CAA	AAG	ATT	CGC	TTT	AGG	GAG	CCA	AGA	GTG	GAT	GAC	AAA	ATT	GTT	912
Pro	Gln	Lys	Ile	Arg	Phe	Arg	Glu	Pro	Arg	Val	Asp	Asp	Lys	Ile	Val	
	290					295					300					
TTG	GTC	AGC	ACA	AAT	TTC	CAG	GAA	AAG	AGT	TCC	TCG	AGC	ACG	GTC	TCA	960
Leu	Val	Ser	Thr	Asn	Phe	Gln	Glu	Lys	Ser	Ser	Ser	Ser	Thr	Val	Ser	
305				310						315					320	
GAG	TCC	AGT	AAC	ATT	TCA	AGA	GTG	CAG	TCA	GCC	AAT	TTC	TAC	AAG	CAT	1008
Glu	Ser	Ser	Asn	Ile	Ser	Arg	Val	Gln	Ser	Ala	Asn	Phe	Tyr	Lys	His	
			325					330						335		
TGG	ATC	TCA	ACA	GTA	GCA	GGA	CAC	TGT	GGA	AAC	CCT	ATG	GTT	TCG	ACT	1056
Trp	Ile	Ser	Thr	Val	Ala	Gly	His	Cys	Gly	Asn	Pro	Met	Val	Ser	Thr	
			340					345					350			
AAA	GAT	GGA	TTT	ATT	GTA	GGT	ATC	CAC	AGT	CTT	GCT	TCA	TTG	ACA	GGC	1104
Lys	Asp	Gly	Phe	Ile	Val	Gly	Ile	His	Ser	Leu	Ala	Ser	Leu	Thr	Gly	
		355					360					365				
GAC	GTT	AAC	ATC	TTC	ACA											

Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile
 195 200 205
 Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Glu Gly His Arg Glu
 210 215 220
 Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His
 225 230 235 240
 Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly
 245 250 255
 Tyr Phe Arg Cys Arg Asn Thr Thr Ser Leu Lys Met Leu Pro Leu Glu
 260 265 270
 Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe
 275 280 285
 Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val
 290 295 300
 Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Ser Thr Val Ser
 305 310 315 320
 Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His
 325 330 335
 Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr
 340 345 350
 Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly
 355 360 365
 Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr
 370 375 380
 Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn
 385 390 395 400
 Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro
 405 410 415
 Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu
 420 425 430
 Asn Cys Ser Phe Gln Ala Ser Ala
 435 440

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCCATGGGG AAAAGTAAGA GAACA

25

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTCTGAGAC CGTGCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGAAAAGAG TTCCTCGAGC

20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTGTTTCAT TCCAAGCACC TGGGCCACCA CCTGGC

36

092440/2424360

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCAGGTGGT GGCCCAGGTG CTTGGAATGA ACAATT

36

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTGTCAGCAC ACCTGGGAGC TGTAGAGCTC

30

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Pro Gly Pro Pro Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Gly Pro Pro Pro Gly Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (H) CELL LINE: KM-102

(vii) IMMEDIATE SOURCE:
 (B) CLONE: KM31-7

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1647
 (D) OTHER INFORMATION:

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 70..1647
 (D) OTHER INFORMATION:

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..69
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG TCA TGT GAG GAC GGT CGG GCC CTG GAA GGA ACG CTC TCG GAA TTG	48
Met Ser Cys Glu Asp Gly Arg Ala Leu Glu Gly Thr Leu Ser Glu Leu	
-23 -20 -15 -10	
GCC GCG GAA ACC GAT CTG CCC GTT GTG TTT GTG AAA CAG AGA AAG ATA	96
Ala Ala Glu Thr Asp Leu Pro Val Val Phe Val Lys Gln Arg Lys Ile	
-5 1 5	
GGC GGC CAT GGT CCA ACC TTG AAG GCT TAT CAG GAG GGC AGA CTT CAA	144
Gly Gly His Gly Pro Thr Leu Lys Ala Tyr Gln Glu Gly Arg Leu Gln	
10 15 20 25	

[illegible]

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Cys Glu Asp Gly Arg Ala Leu Glu Gly Thr Leu Ser Glu Leu
-23 -20 -15 -10

Ala Ala Glu Thr Asp Leu Pro Val Val Phe Val Lys Gln Arg Lys Ile
-5 1 5

Gly Gly His Gly Pro Thr Leu Lys Ala Tyr Gln Glu Gly Arg Leu Gln
10 15 20 25

Lys Leu Leu Lys Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr Asp
30 35 40

Tyr Asp Leu Ile Ile Ile Gly Gly Gly Ser Gly Gly Leu Ala Ala Ala
45 50 55

Lys Glu Ala Ala Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe Val
60 65 70

Thr Pro Thr Pro Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val
75 80 85

Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu
90 95 100 105

Gly Gln Ala Leu Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu
110 115 120

Thr Val Lys His Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His
125 130 135

Ile Gly Ser Leu Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys
140 145 150

Val Val Tyr Glu Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile
155 160 165

Lys Ala Thr Asn Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Arg
170 175 180 185

Phe Leu Ile Ala Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly
190 195 200

Asp Lys Glu Tyr Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr
205 210 215

Cys Pro Gly Lys Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu
220 225 230

Cys Ala Gly Phe Leu Ala Gly Ile Gly Leu Asp Val Thr Val Met Val
235 240 245

Arg Ser Ile Leu Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile
 250 255 260 265
 Gly Glu His Met Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val
 270 275 280
 Pro Ile Lys Val Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg
 285 290 295
 Val Val Ala Gln Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr
 300 305 310
 Asn Thr Val Met Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile
 315 320 325
 Gly Leu Glu Thr Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile
 330 335 340 345
 Pro Val Thr Asp Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile
 350 355 360
 Gly Asp Ile Leu Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln
 365 370 375
 Ala Gly Arg Leu Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys
 380 385 390
 Cys Asp Tyr Glu Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr
 395 400 405
 Gly Ala Cys Gly Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu
 410 415 420 425
 Glu Asn Ile Glu Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr
 430 435 440
 Ile Pro Ser Arg Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn
 445 450 455
 Thr Lys Asp Asn Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn
 460 465 470
 Ala Gly Glu Val Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu
 475 480 485
 Thr Lys Lys Gln Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala
 490 495 500 505
 Glu Val Phe Thr Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile
 510 515 520
 Leu Gln Ala Gly Cys
 525

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAAATAAATA AATAA

15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTAGCGCTCT GGGGCAAGCA TCCTCCAGGC TGGCTGCCAC CACCACCACC ACCACTGATC

60

TAGACT

66

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGTCAGCACA AATTTCCA

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

09442460



24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

18

CATAGGATGC TCCAACAA

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asn Cys Ser Phe Gln Xaa

1

5

THE